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1615  
#8  
Page 1 of 7  
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/960,226

DATE: 01/28/2002

TIME: 13:49:07

Input Set : A:\12243-19SeqLst.txt

Output Set: N:\CRF3\01282002\I960226.raw

3 <110> APPLICANT: Rose, David  
4 Kuntz, Douglas  
5 Van Den Elsen, Jean  
7 <120> TITLE OF INVENTION: MANNOSIDASE STRUCTURES  
9 <130> FILE REFERENCE: 12243.19USU1  
11 <140> CURRENT APPLICATION NUMBER: US 09/960,226  
12 <141> CURRENT FILING DATE: 2001-09-21  
14 <150> PRIOR APPLICATION NUMBER: US 60/263,458  
15 <151> PRIOR FILING DATE: 2001-01-23  
17 <150> PRIOR APPLICATION NUMBER: US 60/234,879  
18 <151> PRIOR FILING DATE: 2000-09-22  
20 <160> NUMBER OF SEQ ID NOS: 9  
22 <170> SOFTWARE: PatentIn version 3.1  
24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 3198  
26 <212> TYPE: DNA  
27 <213> ORGANISM: Drosophila melanogaster  
29 <220> FEATURE:  
30 <221> NAME/KEY: CDS  
31 <222> LOCATION: (1)..(3198)  
32 <223> OTHER INFORMATION:  
35 <400> SEQUENCE: 1

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38 1 5 10 15  
40 ctc ggg aga tct agc cac cat cat cat cat cac gga gaa ttc gac gat 96  
41 Leu Gly Arg Ser Ser His His His His His His Gly Glu Phe Asp Asp  
42 20 25 30  
44 cca ata aga cct cca ctt aaa gtg gct cgt tcc ccg agg cca ggg caa 144  
45 Pro Ile Arg Pro Pro Leu Lys Val Ala Arg Ser Pro Arg Pro Gly Gln  
46 35 40 45  
48 tgc caa gat gtg gtc caa gac gtg ccc aat gtg gat gta cag atg ctg 192  
49 Cys Gln Asp Val Val Gln Asp Val Pro Asn Val Asp Val Gln Met Leu  
50 50 55 60  
52 gag cta tac gat cgc atg tcc ttc aag gac ata gat gga ggc gtg tgg 240  
53 Glu Leu Tyr Asp Arg Met Ser Phe Lys Asp Ile Asp Gly Gly Val Trp  
54 65 70 75 80  
56 aaa cag ggc tgg aac att aag tac gat cca ctg aag tac aac gcc cat 288  
57 Lys Gln Gly Trp Asn Ile Lys Tyr Asp Pro Leu Lys Tyr Asn Ala His  
58 85 90 95  
60 cac aaa cta aaa gtc ttc gtt gtg ccg cac tcg cac aac gat cct gga 336  
61 His Lys Leu Lys Val Phe Val Val Pro His Ser His Asn Asp Pro Gly  
62 100 105 110

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64	tgg att cag acg ttt gag gaa tac tac cag cac gac acc aag cac atc	384
65	Trp Ile Gln Thr Phe Glu Glu Tyr Tyr Gln His Asp Thr Lys His Ile	
66	115 120 125	
68	ctg tcc aat gca cta cgg cat ctg cac gac aat ccc gag atg aag ttc	432
69	Leu Ser Asn Ala Leu Arg His Leu His Asp Asn Pro Glu Met Lys Phe	
70	130 135 140	
72	atc tgg gcg gaa atc tcc tac ttt gct cgg ttc tat cac gat ttg gga	480
73	Ile Trp Ala Glu Ile Ser Tyr Phe Ala Arg Phe Tyr His Asp Leu Gly	
74	145 150 155 160	
76	gag aac aaa aag ctg cag atg aag tcc att gta aag aat gga cag ttg	528
77	Glu Asn Lys Lys Leu Gln Met Lys Ser Ile Val Lys Asn Gly Gln Leu	
78	165 170 175	
80	gaa ttg gaa ttt gtg act gga gga tgg gta atg ccg gac gag gcc aac	576
81	Glu Leu Glu Phe Val Thr Gly Gly Trp Val Met Pro Asp Glu Ala Asn	
82	180 185 190	
84	tcc cac tgg cga aac gta ctg ctg cag ctg acc gaa ggg caa aca tgg	624
85	Ser His Trp Arg Asn Val Leu Leu Gln Leu Thr Glu Gly Gln Thr Trp	
86	195 200 205	
88	ttg aag caa ttc atg aat gtc aca ccc act gct tcc tgg gcc atc gat	672
89	Leu Lys Gln Phe Met Asn Val Thr Pro Thr Ala Ser Trp Ala Ile Asp	
90	210 215 220	
92	ccc ttc gga cac agt ccc act atg ccg tac att ttg cag aag agt ggt	720
93	Pro Phe Gly His Ser Pro Thr Met Pro Tyr Ile Leu Gln Lys Ser Gly	
94	225 230 235 240	
96	ttc aag aat atg ctt atc caa agg acg cac tat tcg gtt aag aag gaa	768
97	Phe Lys Asn Met Leu Ile Gln Arg Thr His Tyr Ser Val Lys Lys Glu	
98	245 250 255	
100	ctg gcc caa cag cga cag ctt gag ttc ctg tgg cgc cag atc tgg gac	816
101	Leu Ala Gln Gln Arg Gln Leu Glu Phe Leu Trp Arg Gln Ile Trp Asp	
102	260 265 270	
104	aac aaa ggg gac aca gct ctc ttc acc cac atg atg ccc ttc tac tcg	864
105	Asn Lys Gly Asp Thr Ala Leu Phe Thr His Met Met Pro Phe Tyr Ser	
106	275 280 285	
108	tac gac att cct cat acc tgt ggt cca gat ccc aag gtt tgc tgt cag	912
109	Tyr Asp Ile Pro His Thr Cys Gly Pro Asp Pro Lys Val Cys Cys Gln	
110	290 295 300	
112	ttc gat ttc aaa cga atg ggc tcc ttc ggt ttg agt tgt cca tgg aag	960
113	Phe Asp Phe Lys Arg Met Gly Ser Phe Gly Leu Ser Cys Pro Trp Lys	
114	305 310 315 320	
116	gtg ccg ccg cgt aca atc agt gat caa aat gtg gca gca cgc tca gat	1008
117	Val Pro Pro Arg Thr Ile Ser Asp Gln Asn Val Ala Ala Arg Ser Asp	
118	325 330 335	
120	ctg ctg gtt gat cag tgg aag aag aag gcc gag ctg tat cgc aca aac	1056
121	Leu Leu Val Asp Gln Trp Lys Lys Lys Ala Glu Leu Tyr Arg Thr Asn	
122	340 345 350	
124	gtg ctg ctg att ccg ttg ggt gac gac ttc cgc ttc aag cag aac acc	1104
125	Val Leu Leu Ile Pro Leu Gly Asp Asp Phe Arg Phe Lys Gln Asn Thr	
126	355 360 365	
128	gag tgg gat gtg cag cgc gtg aac tac gaa agg ctg ttc gaa cac atc	1152

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129	Glu	Trp	Asp	Val	Gln	Arg	Val	Asn	Tyr	Glu	Arg	Leu	Phe	Glu	His	Ile	
130		370					375					380					
132	aac	agc	cag	gcc	cac	ttc	aat	gtc	cag	gcg	cag	ttc	ggc	aca	ctg	cag	1200
133	Asn	Ser	Gln	Ala	His	Phe	Asn	Val	Gln	Ala	Gln	Phe	Gly	Thr	Leu	Gln	
134	385					390					395					400	
136	gaa	tac	ttt	gat	gca	gtg	cac	cag	gcg	gaa	agg	gcg	gga	caa	gcc	gag	1248
137	Glu	Tyr	Phe	Asp	Ala	Val	His	Gln	Ala	Glu	Arg	Ala	Gly	Gln	Ala	Glu	
138					405					410					415		
140	ttt	ccc	acg	cta	agc	ggt	gac	ttt	ttc	aca	tac	gcc	gat	cga	tcg	gat	1296
141	Phe	Pro	Thr	Leu	Ser	Gly	Asp	Phe	Phe	Thr	Tyr	Ala	Asp	Arg	Ser	Asp	
142				420					425					430			
144	aac	tat	tgg	agt	ggc	tac	tac	aca	tcc	cgc	ccg	tat	cat	aag	cgc	atg	1344
145	Asn	Tyr	Trp	Ser	Gly	Tyr	Tyr	Thr	Ser	Arg	Pro	Tyr	His	Lys	Arg	Met	
146			435					440					445				
148	gac	cgc	gtc	ctg	atg	cac	tat	gta	cgt	gca	gca	gaa	atg	ctt	tcc	gcc	1392
149	Asp	Arg	Val	Leu	Met	His	Tyr	Val	Arg	Ala	Ala	Glu	Met	Leu	Ser	Ala	
150		450				455						460					
152	tgg	cac	tcc	tgg	gac	ggt	atg	gcc	cgc	atc	gag	gaa	cgt	ctg	gag	cag	1440
153	Trp	His	Ser	Trp	Asp	Gly	Met	Ala	Arg	Ile	Glu	Glu	Arg	Leu	Glu	Gln	
154	465				470					475						480	
156	gcc	cgc	agg	gag	ctg	tca	ttg	ttc	cag	cac	cac	gac	ggt	ata	act	ggc	1488
157	Ala	Arg	Arg	Glu	Ser	Leu	Phe	Gln	His	His	Asp	Gly	Ile	Thr	Gly		
158				485					490					495			
160	aca	gca	aaa	acg	cac	gta	gtc	gtc	gac	tac	gag	caa	cgc	atg	cag	gaa	1536
161	Thr	Ala	Lys	Thr	His	Val	Val	Val	Asp	Tyr	Glu	Gln	Arg	Met	Gln	Glu	
162				500					505					510			
164	gct	tta	aaa	gcc	tgt	caa	atg	gta	atg	caa	cag	tcg	gtc	tac	cga	ttg	1584
165	Ala	Leu	Lys	Ala	Cys	Gln	Met	Val	Met	Gln	Gln	Ser	Val	Tyr	Arg	Leu	
166			515					520					525				
168	ctg	aca	aag	ccc	tcc	atc	tac	agt	ccg	gac	ttc	agt	ttc	ycg	tac	ttt	1632
169	Leu	Thr	Lys	Pro	Ser	Ile	Tyr	Ser	Pro	Asp	Phe	Ser	Phe	Xaa	Tyr	Phe	
170		530					535					540					
172	acg	ctc	gac	gac	tcc	cgc	tgg	cca	gga	tct	ggt	gtg	gag	gac	agt	cga	1680
173	Thr	Leu	Asp	Asp	Ser	Arg	Trp	Pro	Gly	Ser	Gly	Val	Glu	Asp	Ser	Arg	
174	545					550					555					560	
176	acc	acc	ata	ata	ctg	ggc	gag	gat	ata	ctg	ccc	tcc	aag	cat	gtg	gtg	1728
177	Thr	Thr	Ile	Ile	Leu	Gly	Glu	Asp	Ile	Leu	Pro	Ser	Lys	His	Val	Val	
178					565					570					575		
180	atg	cac	aac	acc	ctg	ccc	cac	tgg	cgg	gag	cag	ctg	gtg	gac	ttt	tat	1776
181	Met	His	Asn	Thr	Leu	Pro	His	Trp	Arg	Glu	Gln	Leu	Val	Asp	Phe	Tyr	
182				580					585					590			
184	gta	tcc	agt	ccg	ttt	gta	agc	gtt	acc	gac	ttg	gca	aac	aat	ccg	gtg	1824
185	Val	Ser	Ser	Pro	Phe	Val	Ser	Val	Thr	Asp	Leu	Ala	Asn	Asn	Pro	Val	
186			595					600					605				
188	gag	gct	cag	gtg	tcc	ccg	gtg	tgg	agc	tgg	cac	cac	gac	aca	ctc	aca	1872
189	Glu	Ala	Gln	Val	Ser	Pro	Val	Trp	Ser	Trp	His	His	Asp	Thr	Leu	Thr	
190		610					615					620					
192	aag	act	atc	cac	cca	caa	ggc	tcc	acc	acc	aag	tac	cgc	atc	atc	ttc	1920
193	Lys	Thr	Ile	His	Pro	Gln	Gly	Ser	Thr	Thr	Lys	Tyr	Arg	Ile	Ile	Phe	

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194	625				630				635				640				
196	aag	gct	cgg	gtg	ccg	ccc	atg	ggc	ttg	gcc	acc	tac	gtt	tta	acc	atc	1968
197	Lys	Ala	Arg	Val	Pro	Pro	Met	Gly	Leu	Ala	Thr	Tyr	Val	Leu	Thr	Ile	
198					645				650					655			
200	tcc	gat	tcc	aag	cca	gag	cac	acc	tcg	tat	gca	tcg	aat	ctc	ttg	ctc	2016
201	Ser	Asp	Ser	Lys	Pro	Glu	His	Thr	Ser	Tyr	Ala	Ser	Asn	Leu	Leu	Leu	
202				660					665					670			
204	cgt	aaa	aac	ccg	act	tcg	tta	cca	ttg	ggc	caa	tat	ccg	gag	gat	gtg	2064
205	Arg	Lys	Asn	Pro	Thr	Ser	Leu	Pro	Leu	Gly	Gln	Tyr	Pro	Glu	Asp	Val	
206			675					680					685				
208	aag	ttt	ggc	gat	cct	cga	gag	atc	tca	ttg	cgg	gtt	ggt	aac	gga	ccc	2112
209	Lys	Phe	Gly	Asp	Pro	Arg	Glu	Ile	Ser	Leu	Arg	Val	Gly	Asn	Gly	Pro	
210		690					695				700						
212	acc	ttg	gcc	ttt	tcg	gag	cag	ggt	ctc	ctt	aag	tcc	att	cag	ctt	act	2160
213	Thr	Leu	Ala	Phe	Ser	Glu	Gln	Gly	Leu	Leu	Lys	Ser	Ile	Gln	Leu	Thr	
214	705					710			715					720			
216	cag	gat	agc	cca	cat	gta	ccg	gtg	cac	ttc	aag	ttc	ctc	aag	tat	ggc	2208
217	Gln	Asp	Ser	Pro	His	Val	Pro	Val	His	Phe	Lys	Phe	Leu	Lys	Tyr	Gly	
218				725					730					735			
220	gtt	cga	tcg	cat	ggc	gat	aga	tcc	ggt	gcc	tat	ctg	ttc	ctg	ccc	aat	2256
221	Val	Arg	Ser	His	Gly	Asp	Arg	Ser	Gly	Ala	Tyr	Leu	Phe	Leu	Pro	Asn	
222				740					745					750			
224	gga	cca	gct	tcg	cca	gtc	gag	ctt	ggc	cag	cca	gtg	gtc	ctg	gtg	act	2304
225	Gly	Pro	Ala	Ser	Pro	Val	Glu	Leu	Gly	Gln	Pro	Val	Val	Leu	Val	Thr	
226			755				760						765				
228	aag	ggc	aaa	ctg	gag	tcg	tcc	gtg	agc	gtg	gga	ctt	ccg	agc	gtg	gtg	2352
229	Lys	Gly	Lys	Leu	Glu	Ser	Ser	Val	Ser	Val	Gly	Leu	Pro	Ser	Val	Val	
230		770				775					780						
232	cac	cag	acg	ata	atg	cgc	ggt	ggt	gca	cct	gag	att	cgc	aat	ctg	gtg	2400
233	His	Gln	Thr	Ile	Met	Arg	Gly	Gly	Ala	Pro	Glu	Ile	Arg	Asn	Leu	Val	
234	785					790					795				800		
236	gat	ata	ggc	tca	ctg	gac	aac	acg	gag	atc	gtg	atg	cgc	ttg	gag	acg	2448
237	Asp	Ile	Gly	Ser	Leu	Asp	Asn	Thr	Glu	Ile	Val	Met	Arg	Leu	Glu	Thr	
238				805					810					815			
240	cat	atc	gac	agc	ggc	gat	atc	ttc	tac	acg	gat	ctc	aat	gga	ttg	caa	2496
241	His	Ile	Asp	Ser	Gly	Asp	Ile	Phe	Tyr	Thr	Asp	Leu	Asn	Gly	Leu	Gln	
242				820					825					830			
244	ttt	atc	aag	agg	cgg	cgt	ttg	gac	aaa	tta	cct	ttg	cag	gcc	aac	tat	2544
245	Phe	Ile	Lys	Arg	Arg	Arg	Leu	Asp	Lys	Leu	Pro	Leu	Gln	Ala	Asn	Tyr	
246			835				840						845				
248	tat	ccc	ata	cct	tcg	ggt	atg	ttc	att	gag	gat	gcc	aat	acg	cga	ctc	2592
249	Tyr	Pro	Ile	Pro	Ser	Gly	Met	Phe	Ile	Glu	Asp	Ala	Asn	Thr	Arg	Leu	
250		850				855					860						
252	act	ctc	ctc	acg	ggt	caa	ccg	ctg	ggt	gga	tct	tct	ctg	gcc	tcg	ggc	2640
253	Thr	Leu	Leu	Thr	Gly	Gln	Pro	Leu	Gly	Gly	Ser	Ser	Leu	Ala	Ser	Gly	
254	865					870					875				880		
256	gag	cta	gag	att	atg	caa	gat	cgt	cgc	ctg	gcc	agc	gat	gat	gaa	cgc	2688
257	Glu	Leu	Glu	Ile	Met	Gln	Asp	Arg	Arg	Leu	Ala	Ser	Asp	Asp	Glu	Arg	
258				885					890						895		

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260 ggc ctg gga cag ggt gtt ttg gac aac aag ccg gtg ctg cat att tat      2736
261 Gly Leu Gly Gln Gly Val Leu Asp Asn Lys Pro Val Leu His Ile Tyr
262          900          905          910
264 cgg ctg gtg ctg gag aag gtt aac aac tgt gtc cga ccg tca aag ctt      2784
265 Arg Leu Val Leu Glu Lys Val Asn Asn Cys Val Arg Pro Ser Lys Leu
266          915          920          925
268 cat cct gcc ggc tat ttg aca agt gcc gca cac aaa gca tcg cag tca      2832
269 His Pro Ala Gly Tyr Leu Thr Ser Ala Ala His Lys Ala Ser Gln Ser
270          930          935          940
272 ctg ctg gat cca ctg gac aag ttt ata ttc gct gaa aat gag tgg atc      2880
273 Leu Leu Asp Pro Leu Asp Lys Phe Ile Phe Ala Glu Asn Glu Trp Ile
274 945          950          955          960
276 ggg gca cag ggg caa ttt ggt ggc gat cat cct tcg gct cgt gag gat      2928
277 Gly Ala Gln Gly Gln Phe Gly Gly Asp His Pro Ser Ala Arg Glu Asp
278          965          970          975
280 ctc gat gtg tcg gtg atg aga cgc tta acc aag agc tcg gcc aaa acc      2976
281 Leu Asp Val Ser Val Met Arg Arg Leu Thr Lys Ser Ser Ala Lys Thr
282          980          985          990
284 cag cga gta ggc tac gtt ctg cac cgc acc aat ctg atg caa tgc ggc      3024
285 Gln Arg Val Gly Tyr Val Leu His Arg Thr Asn Leu Met Gln Cys Gly
286          995          1000          1005
288 act cca gag gag cat aca cag aag ctg gat gtg tgc cac cta ctg      3069
289 Thr Pro Glu Glu His Thr Gln Lys Leu Asp Val Cys His Leu Leu
290          1010          1015          1020
292 ccg aat gtg gcg aga tgc gag gcg acg acg ctg act ttc ctg cag      3114
293 Pro Asn Val Ala Arg Cys Glu Ala Thr Thr Leu Thr Phe Leu Gln
294          1025          1030          1035
296 aat ttg gag cac ttg gat ggc atg gtg gcg ccg gaa gtg tgc ccc      3159
297 Asn Leu Glu His Leu Asp Gly Met Val Ala Pro Glu Val Cys Pro
298          1040          1045          1050
300 atg gaa acc gcc gct tat gtg agc agt cac tca agc tga      3198
301 Met Glu Thr Ala Ala Tyr Val Ser Ser His Ser Ser
302          1055          1060          1065
305 <210> SEQ ID NO: 2
306 <211> LENGTH: 1065
307 <212> TYPE: PRT
308 <213> ORGANISM: Drosophila melanogaster
310 <220> FEATURE:
311 <221> NAME/KEY: misc_feature
312 <222> LOCATION: (542)..(542)
313 <223> OTHER INFORMATION: The 'Xaa' at location 542 stands for Pro, or Ser.
315 <400> SEQUENCE: 2
317 Met Lys Leu Cys Ile Leu Leu Ala Val Val Ala Phe Val Gly Leu Ser
318 1          5          10          15
321 Leu Gly Arg Ser Ser His His His His His His Gly Glu Phe Asp Asp
322          20          25          30
325 Pro Ile Arg Pro Pro Leu Lys Val Ala Arg Ser Pro Arg Pro Gly Gln
326          35          40          45
329 Cys Gln Asp Val Val Gln Asp Val Pro Asn Val Asp Val Gln Met Leu

```

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/960,226

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L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:1189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:1206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9